

7/18
Pur/09/2002

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/719,748

DATE: 06/12/2001
TIME: 11:47:46

Input Set : A:\KIMCHI2A.txt
Output Set: N:\CRF3\06122001\I719748.raw

3 <110> APPLICANT: KIMCHI, Adi
 5 <120> TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
 7 <130> FILE REFERENCE: KIMCHI2A
 9 <140> CURRENT APPLICATION NUMBER: 09/719,748
 10 <141> CURRENT FILING DATE: 2000-12-15
 12 <150> PRIOR APPLICATION NUMBER: 60/089,294
 13 <151> PRIOR FILING DATE: 1998-06-15
 15 <160> NUMBER OF SEQ ID NOS: 14
 17 <170> SOFTWARE: PatentIn Ver. 2.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1742
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Human
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (62)..(1141)
 28 <400> SEQUENCE: 1
 29 gaccgcggca gctcaggcctc ccggccgattt tatgttccag gcctcaatga ggagtccaaa 60
 31 c atg gag cca ttc aag cag cag aag gtg gag gac ttt tat gac atc gga 109
 32 Met Glu Pro Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly
 33 1 5 10 15
 35 gag gag ctg ggg agt ggc cag ttt gcc atc gtg aag aag tgc cgg gag 157
 36 Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg Glu
 37 20 25 30
 39 aag agc acg ggg ctt gag tat gca gcc aag ttc atc aag aag cgg cag 205
 40 Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Gln
 41 35 40 45
 43 agc cgg gcg agc cgg cgc ggt gtg agc cgg gag atc gag cgg gag 253
 44 Ser Arg Ala Ser Arg Arg Gly Val Ser Arg Glu Glu Ile Glu Arg Glu
 45 50 55 60
 47 gtg agc atc ctg cgg cag gtg ctg cac cac aat gtc atc acg ctg cac 301
 48 Val Ser Ile Leu Arg Gln Val Leu His His Asn Val Ile Thr Leu His
 49 65 70 75 80
 51 gac gtc tat gag aac cgc acc gac gtg gtg cac atc ctt gag cta gtg 349
 52 Asp Val Tyr Glu Asn Arg Thr Asp Val Val His Ile Leu Glu Leu Val
 53 85 90 95
 55 tct gga gga gag ctc ttc gat ttc ctg gcc cag aag gag tca ctg agt 397
 56 Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu Ser
 57 100 105 110
 59 gag gag gag gcc acc agc ttc att aag cag atc ctg gat ggg gtg aac 445
 60 Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val Asn
 61 115 120 125
 63 tac ctt cac aca aag aaa att gct cac ttt gat ctc aag cca gaa aac 493
 64 Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu Asn
 65 130 135 140
 67 att atg ttg tta gac aag aat att ccc att cca cac atc aag ctg att 541
 68 Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu Ile

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69	145	150	155	160	
71	gac ttt ggt ctg gct cac gaa ata gaa gat	gga gtt gaa ttt aag aat			589
72	Asp Phe Gly Leu Ala His Glu Ile Glu Asp	Gly Val Glu Phe Lys Asn			
73	165	170	175		
75	att ttt ggg acg ccg gaa ttt gtt gct cca gaa att gtg aac tac gag				637
76	Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu				
77	180	185	190		
79	ccc ctg ggt ctg gag gct gac atg tgg agc ata ggc gtc atc acc tac				685
80	Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr				
81	195	200	205		
83	atc ctc tta agt gga gca tcc cct ttc ctg gga gac acg aag cag gaa				733
84	Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu				
85	210	215	220		
87	aca ctg gca aat atc aca tca gtg agt tac gac ttt gat gag gaa ttc				781
88	Thr Leu Ala Asn Ile Thr Ser Val Ser Tyr Asp Phe Asp Glu Glu Phe				
89	225	230	235	240	
91	ttc agc cat acg agc gag ctg gcc aag gac ttt att cgg aag ctt ctg				829
92	Phe Ser His Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu Leu				
93	245	250	255		
95	gtt aaa gag acc cgg aaa cgg ctc aca atc caa gag gct ctc aga cac				877
96	Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg His				
97	260	265	270		
99	ccc tgg atc acg ccg gtg gac aac cag caa gcc atg gtg cga cgg gag				925
100	Pro Trp Ile Thr Pro Val Asp Asn Gln Gln Ala Met Val Arg Arg Glu				
101	275	280	285		
103	tct gtg gtc aat ctg gag aac ttc agg aag cag tat gtc cgc agg cgg				973
104	Ser Val Val Asn Leu Glu Asn Phe Arg Lys Gln Tyr Val Arg Arg Arg				
105	290	295	300		
107	tgg aag ctt tcc ttc agc atc gtg tcc ctg tgc aac cac ctc acc cgc				1021
108	Trp Lys Leu Ser Phe Ser Ile Val Ser Leu Cys Asn His Leu Thr Arg				
109	305	310	315	320	
111	tcg ctg atg aag aag gtg cac ctg agg ccg gat gag gac ctg agg aac				1069
112	Ser Leu Met Lys Lys Val His Leu Arg Pro Asp Glu Asp Leu Arg Asn				
113	325	330	335		
117	tgt gag agt gac act gag gag gac atc gcc agg agg aaa gcc ctc cac				1117
118	Cys Glu Ser Asp Thr Glu Glu Asp Ile Ala Arg Arg Lys Ala Leu His				
119	340	345	350		
121	cca cgg agg agg agc agc acc tcc taactggcct gacctgcagt ggccgcccagg				1171
122	Pro Arg Arg Arg Ser Ser Thr Ser				
123	355	360			
125	gaggtttggg cccagcgggg ctcccttctg tgcagacttt tggacccagc tcagcaccag				1231
127	caccggggcg tcctgagcac tttgcaagag agatggggccc aaggaattca gaagagctt				1291
129	caggcaagcc aggagaccct gggagctgt gctgtttct gtggaggagg ctccagcatt				1351
131	cccaaagctc ttaattctcc ataaaatggg ctttcctctg tctgccatcc tcagagtctg				1411
133	gggtgggagt gtggacttag gaaaacaata taaaggacat cctcatcatc acggggtaa				1471
135	ggtcagagta aggcagcctt cttcacaggg tgagggggtt cagaaccagc ctggccaaaa				1531
137	attacaccag agagacagag tcctccccat tggAACAGG gtgattgagg aaagtgaacc				1591
139	ttgggtgtga gggaccaatc ctgtgacctc ccagaaccat ggaagccagg acgtcaggct				1651
141	qaccaacacc tcaqacccccc tqaqacqacc cattqctqcc cccqccatqtt qtaattttqcc				1711

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143 tcattttat taaacttctg gtttacctga a 1742
 146 <210> SEQ_ID NO: 2
 147 <211> LENGTH: 360
 148 <212> TYPE: PRT
 149 <213> ORGANISM: Human
 151 <400> SEQUENCE: 2
 152 Met Glu Pro Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly
 153 1 5 10 15
 155 Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg Glu
 156 20 25 30
 158 Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Gln
 159 35 40 45
 161 Ser Arg Ala Ser Arg Arg Gly Val Ser Arg Glu Glu Ile Glu Arg Glu
 162 50 55 60
 164 Val Ser Ile Leu Arg Gln Val Leu His His Asn Val Ile Thr Leu His
 165 65 70 75 80
 167 Asp Val Tyr Glu Asn Arg Thr Asp Val Val His Ile Leu Glu Leu Val
 168 85 90 95
 170 Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu Ser
 171 100 105 110
 173 Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val Asn
 174 115 120 125
 176 Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu Asn
 177 130 135 140
 179 Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu Ile
 180 145 150 155 160
 182 Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys Asn
 183 165 170 175
 185 Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu
 186 180 185 190
 188 Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr
 189 195 200 205
 191 Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu
 192 210 215 220
 194 Thr Leu Ala Asn Ile Thr Ser Val Ser Tyr Asp Phe Asp Glu Glu Phe
 195 225 230 235 240
 197 Phe Ser His Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu Leu
 198 245 250 255
 200 Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg His
 201 260 265 270
 203 Pro Trp Ile Thr Pro Val Asp Asn Gln Gln Ala Met Val Arg Arg Glu
 204 275 280 285
 206 Ser Val Val Asn Leu Glu Asn Phe Arg Lys Gln Tyr Val Arg Arg Arg
 207 290 295 300
 209 Trp Lys Leu Ser Phe Ser Ile Val Ser Leu Cys Asn His Leu Thr Arg
 210 305 310 315 320
 212 Ser Leu Met Lys Lys Val His Leu Arg Pro Asp Glu Asp Leu Arg Asn
 213 325 330 335
 215 Cys Glu Ser Asp Thr Glu Glu Asp Ile Ala Arg Arg Lys Ala Leu His

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216	340	345	350
218	Pro Arg Arg Arg Ser Ser Thr Ser		
219	355	360	
222	<210> SEQ ID NO: 3		
223	<211> LENGTH: 263		
224	<212> TYPE: PRT		
225	<213> ORGANISM: Human		
227	<400> SEQUENCE: 3		
228	Tyr Asp Thr Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Val Val Lys		
229	1 5 10 15		
231	Lys Cys Arg Glu Lys Ser Thr Gly Leu Gln Tyr Ala Ala Lys Phe Ile		
232	20 25 30		
234	Lys Lys Arg Arg Thr Lys Ser Ser Arg Arg Gly Val Ser Arg Glu Asp		
235	35 40 45		
237	Ile Glu Arg Glu Val Ser Ile Leu Lys Glu Ile Gln His Pro Asn Val		
238	50 55 60		
240	Ile Thr Leu His Glu Val Tyr Glu Asn Lys Thr Asp Val Ile Leu Ile		
241	65 70 75 80		
243	Leu Glu Leu Val Ala Gly Gly Glu Leu Phe Asp Phe Leu Ala Glu Lys		
244	85 90 95		
246	Glu Ser Leu Thr Glu Glu Ala Thr Glu Phe Leu Lys Gln Ile Leu		
247	100 105 110		
249	Asn Gly Val Tyr Tyr Leu His Ser Leu Gln Ile Ala His Phe Asp Leu		
250	115 120 125		
252	Lys Pro Glu Asn Ile Met Leu Leu Asp Arg Asn Val Pro Lys Pro Arg		
253	130 135 140		
255	Ile Lys Ile Ile Asp Phe Gly Leu Ala His Lys Ile Asp Phe Gly Asn		
256	145 150 155 160		
258	Glu Phe Lys Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile		
259	165 170 175		
261	Val Asn Tyr Glu Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly		
262	180 185 190		
264	Val Ile Thr Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp		
265	195 200 205		
267	Thr Lys Gln Glu Thr Leu Ala Asn Val Ser Ala Val Asn Tyr Glu Phe		
268	210 215 220		
270	Glu Asp Glu Tyr Phe Ser Asn Thr Ser Ala Leu Ala Lys Asp Phe Ile		
271	225 230 235 240		
273	Arg Arg Leu Leu Val Lys Asp Pro Lys Lys Arg Met Thr Ile Gln Asp		
274	245 250 255		
276	Ser Leu Gln His Pro Trp Ile		
277	260		
280	<210> SEQ ID NO: 4		
281	<211> LENGTH: 263		
282	<212> TYPE: PRT		
283	<213> ORGANISM: Human		
285	<400> SEQUENCE: 4		
286	Tyr Glu Met Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Arg		
287	1 5 10 15		

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289 Lys Cys Arg Gln Lys Gly Thr Gly Lys Glu Tyr Ala Ala Lys Phe Ile
290 20 25 30
292 Lys Lys Arg Arg Leu Ser Ser Ser Arg Arg Gly Val Ser Arg Glu Glu
293 35 40 45
295 Ile Glu Arg Glu Val Asn Ile Leu Arg Glu Ile Arg His Pro Asn Ile
296 50 55 60
298 Ile Thr Leu His Asp Ile Phe Glu Asn Lys Thr Asp Val Val Leu Ile
299 65 70 75 80
301 Leu Glu Leu Val Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Glu Lys
302 85 90 95
304 Glu Ser Leu Thr Glu Asp Glu Ala Thr Gln Phe Leu Lys Gln Ile Leu
305 100 105 110
307 Asp Gly Val His Tyr Leu His Ser Lys Arg Ile Ala His Phe Asp Leu
308 115 120 125
310 Lys Pro Glu Asn Ile Met Leu Leu Asp Lys Asn Val Pro Asn Pro Arg
311 130 135 140
313 Ile Lys Leu Ile Asp Phe Gly Ile Ala His Lys Ile Glu Ala Gly Asn
314 145 150 155 160
316 Glu Phe Lys Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile
317 165 170 175
319 Val Asn Tyr Glu Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly
320 180 185 190
322 Val Ile Thr Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Glu
323 195 200 205
325 Thr Lys Gln Glu Thr Leu Thr Asn Ile Ser Ala Val Asn Tyr Asp Phe
326 210 215 220
328 Asp Glu Glu Tyr Phe Ser Asn Thr Ser Glu Leu Ala Lys Asp Phe Ile
329 225 230 235 240
331 Arg Arg Leu Leu Val Lys Asp Pro Lys Arg Arg Met Thr Ile Ala Gln
332 245 250 255
334 Ser Leu Glu His Ser Trp Ile
335 260
338 <210> SEQ ID NO: 5
339 <211> LENGTH: 261
340 <212> TYPE: PRT
341 <213> ORGANISM: Human
343 <400> SEQUENCE: 5
344 Leu Cys Pro Gly Arg Glu Leu Gly Arg Gly Lys Phe Ala Val Val Arg
345 1 5 10 15
347 Lys Cys Ile Lys Lys Asp Ser Gly Lys Glu Phe Ala Ala Lys Phe Met
348 20 25 30
350 Arg Lys Arg Arg Lys Gly Gln Asp Cys Arg Met Glu Ile Ile His Glu
351 35 40 45
353 Ile Ala Val Leu Glu Leu Ala Gln Asp Asn Pro Trp Val Ile Asn Leu
354 50 55 60
356 His Glu Val Tyr Glu Thr Ala Ser Glu Met Ile Leu Val Leu Glu Tyr
357 65 70 75 80
359 Ala Ala Gly Gly Glu Ile Phe Asp Gln Cys Val Ala Asp Arg Glu Glu
360 85 90 95

VERIFICATION SUMMARY

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